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PC11013

RAW SEQUENCE LISTING

DATE: 02/22/2002

PATENT APPLICATION: US/10/060,521

TIME: 16:06:30

Input Set : A:\PC11013-SEQ-LIST.txt

Output Set: N:\CRF3\02222002\J060521.raw

p#5

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3 <110> APPLICANT: Mueller, John P.
4      Baima, Eric T.
6 <120> TITLE OF INVENTION: HAR A NUCLEIC ACIDS, POLYPEPTIDES, AND RELATED METHODS
7      AND USES THEREOF
9 <130> FILE REFERENCE: PC11013
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/060,521
C--> 12 <141> CURRENT FILING DATE: 2002-01-30
14 <160> NUMBER OF SEQ ID NOS: 10
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1497
20 <212> TYPE: DNA
21 <213> ORGANISM: Enterococcus faecalis
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25 tttgatcagg caaatatcac gatggatacc aattggaaat taggattgat tggccgcaat 120
26 ggccgtggga aaacaacctt attaagattg ttacaaaaaac agttggatta ccaaggagag 180
27 attcttcatc aagtcgattt cgtctatttt ccacaaacag ttgcagaaga acaacagctc 240
28 acttattatg tcttacaaga ggtgacttct tttgaacagt gggaattaga acgagaatta 300
29 acgcttttaa acgttgatcc tgaagtttta tggcggccct tttcttcttt atcaggcggc 360
30 gaaaagacga aagttttatt aggtcttctt tttattgaag aaaatgcctt tcctttaatt 420
31 gacgagccaa caaatcattt agatctagct ggcagacaac aagtggctga atatttgaag 480
32 aaaaagaaac acgggtttat tttagtcagc cacgatcggg catttggtga tgaagtgggt 540
33 gatcatattt tggcgattga aaaaagtcaa ttgacgctgt atcaaggga tttttctatt 600
34 tatgaagagc aaaaaaaatt aagagatgct tttgaactag cagaaaaatga aaaaatcaaa 660
35 aaagaagtca atcgcttgaa agaaaccgct cgtaaaaaag cggaatggtc gatgaaccgt 720
36 gaaggtgata agtacggcaa cgctaaggaa aaagggagcg gggcgatttt tgatacagga 780
37 gccattggtg cccgggcagc gcgcgtaatg aagcgctcga aacacattca acaacgcgcc 840
38 gaaacacaat tagcagaaaa agaaaaacta ttaaaagatc ttgagtatat tgatcctttg 900
39 tcaatggatt atcagccaac gcatcacaaa acattattga cggtggaaga gcttcgtcta 960
40 ggctacgaga aaaattggct atttgcgcca ctttcttttt caataaacgc gggagaaatt 1020
41 gttggaataa cagggaaaaa tggctcagga aaatcgagct taattcagta tttattggat 1080
42 aatttttctg gggattcaga aggcgaagcc actttggctc accaattaac catttcttat 1140
43 gtgcgccaag attatgaaga caatcaagga actttatccg aatttgcaga gaaaaatcag 1200
44 ttagattaca ctcaattttt aaataactta cgaaaaactg ggatggagcg cgccgttttc 1260
45 actaatcgaa ttgaacaaaat gagtatgggg caacggaaaa aagtcgaagt agccaaatca 1320
46 ttgtctcaat cagctgaact ttatatgttg gatgaacccc ttaattactt ggatgtattt 1380
47 aatcatcaac aattagaagc gctaattctt tctgtgaagc ctgcaatgct agtgattgag 1440
48 catgatgcac atttcatgaa gaaaataaca gataaaaaaa ttgtcttgaa atcataa 1497
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 498
53 <212> TYPE: PRT
54 <213> ORGANISM: Enterococcus faecalis

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56 <400> SEQUENCE: 2

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58   1           5           10           15
60 Glu Val Leu Leu Phe Asp Gln Ala Asn Ile Thr Met Asp Thr Asn Trp
61           20           25           30
63 Lys Leu Gly Leu Ile Gly Arg Asn Gly Arg Gly Lys Thr Thr Leu Leu
64           35           40           45
66 Arg Leu Leu Gln Lys Gln Leu Asp Tyr Gln Gly Glu Ile Leu His Gln
67           50           55           60
69 Val Asp Phe Val Tyr Phe Pro Gln Thr Val Ala Glu Glu Gln Gln Leu
70   65           70           75           80
72 Thr Tyr Tyr Val Leu Gln Glu Val Thr Ser Phe Glu Gln Trp Glu Leu
73           85           90           95
75 Glu Arg Glu Leu Thr Leu Leu Asn Val Asp Pro Glu Val Leu Trp Arg
76           100          105          110
78 Pro Phe Ser Ser Leu Ser Gly Gly Glu Lys Thr Lys Val Leu Leu Gly
79           115          120          125
81 Leu Leu Phe Ile Glu Glu Asn Ala Phe Pro Leu Ile Asp Glu Pro Thr
82           130          135          140
84 Asn His Leu Asp Leu Ala Gly Arg Gln Gln Val Ala Glu Tyr Leu Lys
85 145          150          155          160
87 Lys Lys Lys His Gly Phe Ile Leu Val Ser His Asp Arg Ala Phe Val
88           165          170          175
90 Asp Glu Val Val Asp His Ile Leu Ala Ile Glu Lys Ser Gln Leu Thr
91           180          185          190
93 Leu Tyr Gln Gly Asn Phe Ser Ile Tyr Glu Glu Gln Lys Lys Leu Arg
94           195          200          205
96 Asp Ala Phe Glu Leu Ala Glu Asn Glu Lys Ile Lys Lys Glu Val Asn
97           210          215          220
99 Arg Leu Lys Glu Thr Ala Arg Lys Lys Ala Glu Trp Ser Met Asn Arg
100 225          230          235          240
102 Glu Gly Asp Lys Tyr Gly Asn Ala Lys Glu Lys Gly Ser Gly Ala Ile
103           245          250          255
105 Phe Asp Thr Gly Ala Ile Gly Ala Arg Ala Ala Arg Val Met Lys Arg
106           260          265          270
108 Ser Lys His Ile Gln Gln Arg Ala Glu Thr Gln Leu Ala Glu Lys Glu
109           275          280          285
111 Lys Leu Leu Lys Asp Leu Glu Tyr Ile Asp Pro Leu Ser Met Asp Tyr
112           290          295          300
114 Gln Pro Thr His His Lys Thr Leu Leu Thr Val Glu Glu Leu Arg Leu
115 305          310          315          320
117 Gly Tyr Glu Lys Asn Trp Leu Phe Ala Pro Leu Ser Phe Ser Ile Asn
118           325          330          335
120 Ala Gly Glu Ile Val Gly Ile Thr Gly Lys Asn Gly Ser Gly Lys Ser
121           340          345          350
123 Ser Leu Ile Gln Tyr Leu Leu Asp Asn Phe Ser Gly Asp Ser Glu Gly
124           355          360          365
126 Glu Ala Thr Leu Ala His Gln Leu Thr Ile Ser Tyr Val Arg Gln Asp
127           370          375          380

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129 Tyr Glu Asp Asn Gln Gly Thr Leu Ser Glu Phe Ala Glu Lys Asn Gln
 130 385 390 395 400
 132 Leu Asp Tyr Thr Gln Phe Leu Asn Asn Leu Arg Lys Leu Gly Met Glu
 133 405 410 415
 135 Arg Ala Val Phe Thr Asn Arg Ile Glu Gln Met Ser Met Gly Gln Arg
 136 420 425 430
 138 Lys Lys Val Glu Val Ala Lys Ser Leu Ser Gln Ser Ala Glu Leu Tyr
 139 435 440 445
 141 Ile Trp Asp Glu Pro Leu Asn Tyr Leu Asp Val Phe Asn His Gln Gln
 142 450 455 460
 144 Leu Glu Ala Leu Ile Leu Ser Val Lys Pro Ala Met Leu Val Ile Glu
 145 465 470 475 480
 147 His Asp Ala His Phe Met Lys Lys Ile Thr Asp Lys Lys Ile Val Leu
 148 485 490 495
 150 Lys Ser

154 <210> SEQ ID NO: 3

155 <211> LENGTH: 1644

156 <212> TYPE: DNA

157 <213> ORGANISM: Bacillus subtilis

159 <400> SEQUENCE: 3

160 atgaaagaga tcgtaacatt aacaaacggt agctatgaag taaaggatca aactgttttt 60
 161 aaacatgtaa acgccagtgt tcagcaagga gatatacatt ggattatcgg caaaaacggc 120
 162 gctgggaaat ctacgttgct gcacctcatt cacaatgact tagcccctgc acagggtcaa 180
 163 atccttcgga aggatataaaa actggctttg gttgaacagg aaaccgcggc gtattccttt 240
 164 gcggatcaga cacctgccga aaagaagtta ctggagaaat ggcatgtgcc tcttcgtgat 300
 165 ttctcatcgt taagcggcgg tgaaaaactg aaagcgcggc tggcgaaagg actatcagag 360
 166 gatgcagatc tgctgctggt agatgaaccg acaaaccacc ttgatgaaaa aagcttgcaa 420
 167 ttctcatccc aacagctgaa acattataac ggcaactgtga ttctcgtttc tcacgatcga 480
 168 tatttttttag acgaagccgc aacaaaaata tggctcgcttg aggatcagac gctgattgaa 540
 169 ttcaaaggga attactccgg gtatatgaag ttccgggaga agaaaagact caccagcag 600
 170 cgtgaatatg aaaagcagca aaaaatggtt gaacggattg aagcacaaat gaatgggctc 660
 171 gcttcttggt cgaaaaagc ccatgctcaa tcgacgaaaa aggaagggtt taaagaatat 720
 172 caccgggtaa aagcgaagcg tacggatgcc cagataaaat ccaagcagaa gcggcttgaa 780
 173 aaagagcttg aaaaagcaaa ggcggaaccc gttaccccag aatatacagt ccgcttttca 840
 174 atcgatacaa cccacaaaac aggaaaacgt tttttagaag ttcagaatgt aacaaaagcg 900
 175 ttggagaaaa ggactctctt taaaaacgca aactttacaa ttcagcacgg cgaaaagggt 960
 176 gcgatcatag gcccgaatgg cagcggaaaa acgacattac tgaacatcat tctgggacag 1020
 177 gaaacagcag aaggaagtgt atgggtgtcg cgtccgcaa acatcggcta tttaacgcag 1080
 178 gaggtgtttg atttgctttt agaacaaaca ccggaagagt tatttgagaa tgaaacattc 1140
 179 aaagcaaggg ggcacgttca aaatctgatg aggcacttag gttttacagc cgcccgaatg 1200
 180 actgaaccga tcaagcatat gagtatgggt gagcgtgtaa agatcaagct gatggcatat 1260
 181 attctggagg aaaaagacgt gctgatttta gatgagccga caaacatct cgacctgccg 1320
 182 tcacgcgaac agctggaaga aacactgtca caatacagcg gcacattgct ggcggtttca 1380
 183 catgaccgat actttctcga aaaaacaaca aacagtaaac tcgtcatctc aaacaacggc 1440
 184 atcgaaaaagc agttaaacga cgttccttca gaaagaaatg agcgggagga gcttcggtta 1500
 185 aagcttgaga cagaaagaca agaagtgtct ggaaagctca gttttatgac gccaaatgat 1560
 186 aaaggggtata aggagcttga tcaggctttc aatgagctta cgaaacgaat aaaagagctg 1620
 187 gatcatcaag acaaaaaaga ctga 1644
 190 <210> SEQ ID NO: 4

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191 <211> LENGTH: 547
192 <212> TYPE: PRT
193 <213> ORGANISM: Bacillus subtilis
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200           20           25           30
202 Ile Gly Ile Ile Gly Lys Asn Gly Ala Gly Lys Ser Thr Leu Leu His
203           35           40           45
205 Leu Ile His Asn Asp Leu Ala Pro Ala Gln Gly Gln Ile Leu Arg Lys
206           50           55           60
208 Asp Ile Lys Leu Ala Leu Val Glu Gln Glu Thr Ala Ala Tyr Ser Phe
209   65           70           75           80
211 Ala Asp Gln Thr Pro Ala Glu Lys Lys Leu Leu Glu Lys Trp His Val
212           85           90           95
214 Pro Leu Arg Asp Phe His Gln Leu Ser Gly Gly Glu Lys Leu Lys Ala
215           100          105          110
217 Arg Leu Ala Lys Gly Leu Ser Glu Asp Ala Asp Leu Leu Leu Leu Asp
218           115          120          125
220 Glu Pro Thr Asn His Leu Asp Glu Lys Ser Leu Gln Phe Leu Ile Gln
221           130          135          140
223 Gln Leu Lys His Tyr Asn Gly Thr Val Ile Leu Val Ser His Asp Arg
224  145          150          155          160
226 Tyr Phe Leu Asp Glu Ala Ala Thr Lys Ile Trp Ser Leu Glu Asp Gln
227           165          170          175
229 Thr Leu Ile Glu Phe Lys Gly Asn Tyr Ser Gly Tyr Met Lys Phe Arg
230           180          185          190
232 Glu Lys Lys Arg Leu Thr Gln Gln Arg Glu Tyr Glu Lys Gln Gln Lys
233           195          200          205
235 Met Val Glu Arg Ile Glu Ala Gln Met Asn Gly Leu Ala Ser Trp Ser
236           210          215          220
238 Glu Lys Ala His Ala Gln Ser Thr Lys Lys Glu Gly Phe Lys Glu Tyr
239  225          230          235          240
241 His Arg Val Lys Ala Lys Arg Thr Asp Ala Gln Ile Lys Ser Lys Gln
242           245          250          255
244 Lys Arg Leu Glu Lys Glu Leu Glu Lys Ala Lys Ala Glu Pro Val Thr
245           260          265          270
247 Pro Glu Tyr Thr Val Arg Phe Ser Ile Asp Thr Thr His Lys Thr Gly
248           275          280          285
250 Lys Arg Phe Leu Glu Val Gln Asn Val Thr Lys Ala Phe Gly Glu Arg
251           290          295          300
253 Thr Leu Phe Lys Asn Ala Asn Phe Thr Ile Gln His Gly Glu Lys Val
254  305          310          315          320
256 Ala Ile Ile Gly Pro Asn Gly Ser Gly Lys Thr Thr Leu Leu Asn Ile
257           325          330          335
259 Ile Leu Gly Gln Glu Thr Ala Glu Gly Ser Val Trp Val Ser Pro Ser
260           340          345          350
262 Ala Asn Ile Gly Tyr Leu Thr Gln Glu Val Phe Asp Leu Pro Leu Glu

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263          355          360          365
265 Gln Thr Pro Glu Glu Leu Phe Glu Asn Glu Thr Phe Lys Ala Arg Gly
266          370          375          380
268 His Val Gln Asn Leu Met Arg His Leu Gly Phe Thr Ala Ala Gln Trp
269 385          390          395          400
271 Thr Glu Pro Ile Lys His Met Ser Met Gly Glu Arg Val Lys Ile Lys
272          405          410          415
274 Leu Met Ala Tyr Ile Leu Glu Glu Lys Asp Val Leu Ile Leu Asp Glu
275          420          425          430
277 Pro Thr Asn His Leu Asp Leu Pro Ser Arg Glu Gln Leu Glu Glu Thr
278          435          440          445
280 Leu Ser Gln Tyr Ser Gly Thr Leu Leu Ala Val Ser His Asp Arg Tyr
281          450          455          460
283 Phe Leu Glu Lys Thr Thr Asn Ser Lys Leu Val Ile Ser Asn Asn Gly
284 465          470          475          480
286 Ile Glu Lys Gln Leu Asn Asp Val Pro Ser Glu Arg Asn Glu Arg Glu
287          485          490          495
289 Glu Leu Arg Leu Lys Leu Glu Thr Glu Arg Gln Glu Val Leu Gly Lys
290          500          505          510
292 Leu Ser Phe Met Thr Pro Asn Asp Lys Gly Tyr Lys Glu Leu Asp Gln
293          515          520          525
295 Ala Phe Asn Glu Leu Thr Lys Arg Ile Lys Glu Leu Asp His Gln Asp
296          530          535          540
298 Lys Lys Asp
299 545
302 <210> SEQ ID NO: 5
303 <211> LENGTH: 22
304 <212> TYPE: DNA
305 <213> ORGANISM: Enterococcus faecalis
307 <400> SEQUENCE: 5
308 tctagatatc acgatggata cc                                22
311 <210> SEQ ID NO: 6
312 <211> LENGTH: 23
313 <212> TYPE: DNA
314 <213> ORGANISM: Enterococcus faecalis
316 <400> SEQUENCE: 6
317 tctagattgc cgtacttatac acc                                23
320 <210> SEQ ID NO: 7
321 <211> LENGTH: 31
322 <212> TYPE: DNA
323 <213> ORGANISM: Bacillus subtilis
325 <400> SEQUENCE: 7
326 catatgaaag agatcgtaac attaacaaac g                        31
329 <210> SEQ ID NO: 8
330 <211> LENGTH: 31
331 <212> TYPE: DNA
332 <213> ORGANISM: Bacillus subtilis
334 <400> SEQUENCE: 8
335 ggatccttag tcttttttgt cttgatgatc c                        31

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/060,521

DATE: 02/22/2002

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Input Set : A:\PC11013-SEQ-LIST.txt

Output Set: N:\CRF3\02222002\J060521.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date